STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/521,478_
Source: _PU7/10_
Date Processed by STIC: _1/28/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
**http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/521,478_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ **Wrapped Nucleics**
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

•2 ___ **Invalid Line Length** — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ **Misaligned Amino Numbering** — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ **Non-ASCII** — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ **Variable Length** — Sequence(s)___contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ **PatentIn 2.0 "bug"** — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ **Skipped Sequences (OLD RULES)** — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ **Skipped Sequences (NEW RULES)** — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ **Use of n's or Xaa's (NEW RULES)** — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ **Invalid <213> Response** — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ **Use of <220>** — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ **PatentIn 2.0 "bug"** — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ **Misuse of n/Xaa** — "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>
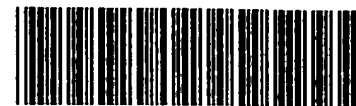
PCT

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                RAW SEQUENCE LISTING            DATE: 01/28/2005
                PATENT APPLICATION:  US/10/521,478   TIME: 11:37:36

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                Output Set: N:\CRF4\01282005\J521478.raw

      4 <110> APPLICANT: Michel, Albrecht
      5         Scheffler, Brian E.
      6         Netherland, Michael D.
      7         Dayan, Franck E.
      8         Arias de Ares, Renee S.
     10 <120> TITLE OF INVENTION: HERBICIDE-RESISTANT PLANTS, AND POLYNUCLEOTIDES AND
     11         METHODS FOR PROVIDING SAME
W--> 13 <130> FILE REFERENCE:
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/521,478
C--> 16 <141> CURRENT FILING DATE: 2005-01-17
     18 <160> NUMBER OF SEQ ID NOS: 8
     20 <170> SOFTWARE: PatentIn Ver. 2.1


ERRORED SEQUENCES

     22 <210> SEQ ID NO: 1
     23 <211> LENGTH: 1982
     24 <212> TYPE: DNA
     25 <213> ORGANISM: Hydrilla verticillata
     27 <220> FEATURE:
     28 <221> NAME/KEY: CDS
     29 <222> LOCATION: (6)..(1748)
     31 <400> SEQUENCE: 1
E--> 32 caaac atg act gtt gct agg tcg gtc gtt gca gtc aat cta agt ggt tcc  50
     33 50
     34       Met Thr Val Ala Arg Ser Val Val Ala Val Asn Leu Ser Gly Ser
     35        1               5              10              15
E--> 37 ctt caa aac aga tac cca gcc agt tca tca gtc agc tgc ttc ctt ggc  98
     38 98
     39 Leu Gln Asn Arg Tyr Pro Ala Ser Ser Ser Val Ser Cys Phe Leu Gly
     40            20              25              30
E--> 42 aaa gag tac aga tgc aac agt atg tta gga ttc tgc ggt agt gga aaa
     43 146
     44 Lys Glu Tyr Arg Cys Asn Ser Met Leu Gly Phe Cys Gly Ser Gly Lys
     45            35              40              45
E--> 47 ttg gct ttt ggc gca aat gca ccc tat tct aag att gca gct acc aaa
     48 194
     49 Leu Ala Phe Gly Ala Asn Ala Pro Tyr Ser Lys Ile Ala Ala Thr Lys
     50            50              55              60
E--> 52 cca aag ccc aaa ctt cgc cct ttg aag gtc aac tgc atg gat ttc cca
     53 242
     54 Pro Lys Pro Lys Leu Arg Pro Leu Lys Val Asn Cys Met Asp Phe Pro
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        55        65                    70                   75
E--> 59 aga cct gat ata gat aac act gct aat ttc ttg gaa gct gct gct ctt
     60 290
     61 Arg Pro Asp Ile Asp Asn Thr Ala Asn Phe Leu Glu Ala Ala Ala Leu
     62  80                    85                   90                   95
E--> 64 tct tcc tct ttt cgc aat tca gca aga cca agt aaa cct ctt caa gtt
     65 338
     66 Ser Ser Ser Phe Arg Asn Ser Ala Arg Pro Ser Lys Pro Leu Gln Val
     67                   100                  105                  110
E--> 69 gta att gct ggt gca ggt ttg gct ggt ctt tca aca gca aag tat ctc
     70 386
     71 Val Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr Leu
     72                   115                  120                  125
E--> 74 gca gat gca ggg cac ata ccc ata cta ctg gag gct aga gat gta ttg
     75 434
     76 Ala Asp Ala Gly His Ile Pro Ile Leu Leu Glu Ala Arg Asp Val Leu
     77             130                  135                  140
E--> 79 ggt ggc aag gtg gca gcg tgg aaa gat gat gat gga gac tgg tat gag
     80 482
     81 Gly Gly Lys Val Ala Ala Trp Lys Asp Asp Asp Gly Asp Trp Tyr Glu
     82     145                  150                  155
E--> 84 aca ggc ctg cat ata ttt ttt ggt gca tat ccc aat gtg cag aat tta
     85 530
     86 Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Val Gln Asn Leu
     87 160                  165                  170                  175
E--> 89 ttt ggt gaa ctt ggc ata aat gat cgt cta caa tgg aaa gag cat tca
     90 578
     91 Phe Gly Glu Leu Gly Ile Asn Asp Arg Leu Gln Trp Lys Glu His Ser
     92                   180                  185                  190
E--> 94 atg att ttt gcg atg cca aac aag cca ggg gaa ttt agt cgc ttt gat
     95 626
     96 Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser Arg Phe Asp
     97             195                  200                  205
E--> 99 ttt cca gaa gta ctt cct gct cca cta aat gga ata tgg gca atc ctt
    100 674
    101 Phe Pro Glu Val Leu Pro Ala Pro Leu Asn Gly Ile Trp Ala Ile Leu
    102             210                  215                  220
E--> 104 aaa aac aat gaa atg ctc act tgg cca gag aaa gtg caa ttt gct att
    105 722
    106 Lys Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Gln Phe Ala Ile
    107     225                  230                  235
E--> 109 gga cta cta cct gca atg att ggg ggg cag cca tat gtt gaa gct cag
    110 770
    111 Gly Leu Leu Pro Ala Met Ile Gly Gly Gln Pro Tyr Val Glu Ala Gln
    112 240                  245                  250                  255
E--> 116 gat ggc tta aca gtt caa gag tgg atg aga aaa cag ggt gtg ccg gat
    117 818
    118 Asp Gly Leu Thr Val Gln Glu Trp Met Arg Lys Gln Gly Val Pro Asp
    119                   260                  265                  270
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same error (handwritten annotation)

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E--> 121 cga gtc aat gac gag gtt ttc att gca atg tca aag gct ctt aac ttc
     122 866
     123 Arg Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn Phe
     124             275             280             285
E--> 126 ata aac cct gat gaa ctt tcc atg caa tgc atc ctg att gcc tta aac
     127 914
     128 Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu Asn
     129         290             295             300
E--> 131 cgt ttc ctt cag gaa aag cat ggg tcg aag atg gcc ttt tta gat ggt
     132 962
     133 Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp Gly
     134         305             310             315
E--> 136 aat cca cct gaa aga tta tgt aag cca att gct gat cac atc gag tca
     137 1010
     138 Asn Pro Pro Glu Arg Leu Cys Lys Pro Ile Ala Asp His Ile Glu Ser
     139 320             325             330                 335
E--> 141 ttg ggt ggc caa gtc atc ctt aat tcc cga ata cag aag att gag ctg
     142 1058
     143 Leu Gly Gly Gln Val Ile Leu Asn Ser Arg Ile Gln Lys Ile Glu Leu
     144             340             345             350
E--> 146 aat gca gac aaa tcc gtc aag cat ttt gtg ctc acc aat gga aat ata
     147 1106
     148 Asn Ala Asp Lys Ser Val Lys His Phe Val Leu Thr Asn Gly Asn Ile
     149             355             360             365
E--> 151 ata aca gga gat gca tat gta ttt gca aca cct gtt gat atc ttg aag
     152 1154
     153 Ile Thr Gly Asp Ala Tyr Val Phe Ala Thr Pro Val Asp Ile Leu Lys
     154             370             375             380
E--> 156 ctt ctg tta cct gaa gat tgg aag gag att tca tat ttc aaa aaa ttg
     157 1202
     158 Leu Leu Leu Pro Glu Asp Trp Lys Glu Ile Ser Tyr Phe Lys Lys Leu
     159         385             390             395
E--> 161 gac aag ttg gtt ggc gta cct gtg ata aat gta cac ata tgg ttt gat
     162 1250
     163 Asp Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe Asp
     164 400             405             410             415
E--> 166 agg aag ttg aag aac aca tac gat cat ctt ctt ttc agc agg agt cca
     167 1298
     168 Arg Lys Leu Lys Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser Pro
     169             420             425             430
E--> 173 ctg ttg agc gtt tat gca gac atg tct gtt aca tgc aag gaa tac tac
     174 1346
     175 Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr Tyr
     176             435             440             445
E--> 178 aat cca aat caa tcc atg ctt gag cta gta ttt gca cca gca gag aaa
     179 1394
     180 Asn Pro Asn Gln Ser Met Leu Glu Leu Val Phe Ala Pro Ala Glu Lys
     181         450             455             460
E--> 183 tgg att tca tgc agt gac agt gaa atc att aac gcg act atg caa gag
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        184 1442
        185 Trp Ile Ser Cys Ser Asp Ser Glu Ile Ile Asn Ala Thr Met Gln Glu
        186     465                 470                 475
E--> 188 ctt gct aaa ctc ttt cca gat gag att tct gct gat caa agc aag gcc
        189 1490
        190 Leu Ala Lys Leu Phe Pro Asp Glu Ile Ser Ala Asp Gln Ser Lys Ala
        191 480                 485                 490                 495
E--> 193 aaa att ttg aaa tat cat gtt gta aag acc ccg agg tca gtt tac aag
        194 1538
        195 Lys Ile Leu Lys Tyr His Val Val Lys Thr Pro Arg Ser Val Tyr Lys
        196                 500                 505                 510
E--> 198 acg gtc cct gat tgt gaa cca tgc cgg cct ttg caa aga tct cca att
        199 1586
        200 Thr Val Pro Asp Cys Glu Pro Cys Arg Pro Leu Gln Arg Ser Pro Ile
        201             515                 520                 525
E--> 203 gaa ggg ttc tac ttg gct ggt gac tac aca aag cag aag tat ttg gcc
        204 1634
        205 Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu Ala
        206             530                 535                 540
E--> 208 tca atg gaa ggt gcc gtg tta tct ggg aag cta tgt gct cag gca att
        209 1682
        210 Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ala Ile
        211     545                 550                 555
E--> 213 gtg cag gac tgc agc ttg ttg gct tct agg gta cag aaa agc cca cag
        214 1730
        215 Val Gln Asp Cys Ser Leu Leu Ala Ser Arg Val Gln Lys Ser Pro Gln
        216 560                 565                 570                 575
E--> 218 acg ttg acg att gcc tga ttcaggaaac ttttatgcag gttcagtttg
        219 1778
        220 Thr Leu Thr Ile Ala
        221                 580
E--> 223 taggggggaat atttctggtt ttgtttcatt cagatgtttt tcttttagag catatgtctt
        224 1838
E--> 226 tatagtaaaa actcccacct ctttctcatg tatagctaca tcagcaagca aaggggggtaa
        227 1898
E--> 231 gttgcaattt caggacttga acatggcctc tgcacaggta aagacagaat ggacataaat
        232 1958
E--> 234 gcaagcatgg aatttacaat attc
        235 1982
        323 <210> SEQ ID NO: 3
        324 <211> LENGTH: 2293
        325 <212> TYPE: DNA
        326 <213> ORGANISM: Glycine max
        328 <220> FEATURE:
        329 <221> NAME/KEY: CDS
        330 <222> LOCATION: (221)..(1933)
        332 <400> SEQUENCE: 3
E--> 333 gaattccttc tacgtactgc cgtggtgctt tcaccactgc ttaccactaa ccttcctctc
        334 60
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same

same

●   ●

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E--> 336 tctctctgcc gctgcaagct tggtactctc aactcaattc tccaccttat tcttttcact
    337 120
E--> 339 tcttcagctc ttgttttttc ccaaatctac tttcaaagtg cctgaattct gcaacagtaa
    340 180
E--> 342 tattaacact cctctctttt gttcaggctt tatttcccca atg gcc gct tgt ggc
    343 235
    344                                                 Met Ala Ala Cys Gly
    347                                                  1               5
E--> 349 tat ata tct gct gcc aac ttc aat tat ctc gtt ggc gcc aga aac ata
    350 283
    351 Tyr Ile Ser Ala Ala Asn Phe Asn Tyr Leu Val Gly Ala Arg Asn Ile
    352                   10                  15                  20
E--> 354 tcc aaa ttc gct tct tca gac gcc aca att tcg ttt tca ttt ggc ggg
    355 331
    356 Ser Lys Phe Ala Ser Ser Asp Ala Thr Ile Ser Phe Ser Phe Gly Gly
    357                   25                  30                  35
E--> 359 agc gac tca atg ggt ctt act ttg cga ccc gct ccg att cgt gct cct
    360 379
    361 Ser Asp Ser Met Gly Leu Thr Leu Arg Pro Ala Pro Ile Arg Ala Pro
    362                   40                  45                  50
E--> 364 aag agg aac cat ttc tct ccc ttg cgt gtc gtt tgc gtc gat tat cca
    365 427
    366 Lys Arg Asn His Phe Ser Pro Leu Arg Val Val Cys Val Asp Tyr Pro
    367         55                  60                  65
E--> 369 cgc cca gag ctc gaa aac acc gtt aat ttc gtt gaa gct gct tac ttg
    370 475
    371 Arg Pro Glu Leu Glu Asn Thr Val Asn Phe Val Glu Ala Ala Tyr Leu
    372 70                  75                  80                  85
E--> 374 tct tcc acc ttt cgt gct tct ccg cgt cct cta aaa ccc ttg aac atc
    375 523
    376 Ser Ser Thr Phe Arg Ala Ser Pro Arg Pro Leu Lys Pro Leu Asn Ile
    377                   90                  95                  100
E--> 379 gtt att gcc ggt gca gga ttg gct ggt tta tca act gca aaa tat ttg
    380 571
    381 Val Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr Leu
    382                   105                 110                 115
E--> 384 gct gat gct ggg cat aaa cct ata ttg ctg gaa gca aga gac gtt cta
    385 619
    386 Ala Asp Ala Gly His Lys Pro Ile Leu Leu Glu Ala Arg Asp Val Leu
    387         120                 125                 130
E--> 389 ggt gga aag gtt gct gca tgg aaa gac aag gat gga gac tgg tac gag
    390 667
    391 Gly Gly Lys Val Ala Ala Trp Lys Asp Lys Asp Gly Asp Trp Tyr Glu
    392         135                 140                 145
E--> 394 aca ggc cta cac atc ttt ttt ggg gct tac cct tat gtg cag aac ctt
    395 715
    396 Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Tyr Val Gln Asn Leu
    397 150                 155                 160                 165
E--> 399 ttt gga gaa ctt ggc att aat gat cgg tta caa tgg aaa gag cat tct
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same

● ●

RAW SEQUENCE LISTING   DATE: 01/28/2005
PATENT APPLICATION: US/10/521,478   TIME: 11:37:36

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Output Set: N:\CRF4\01282005\J521478.raw

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E--> 406 atg att ttt gct atg cca aat aag cct gga gag ttt agt cga ttt gat
         407 811
         408 Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser Arg Phe Asp
         409             185             190             195
E--> 411 ttt cct gaa gtt ctt ccc tcc cca ttg aat gga ata tgg gca ata ttg
         412 859
         413 Phe Pro Glu Val Leu Pro Ser Pro Leu Asn Gly Ile Trp Ala Ile Leu
         414         200             205             210
E--> 416 agg aac aat gag atg ctt aca tgg cca gag aaa gta aaa ttt gca att
         417 907
         418 Arg Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Lys Phe Ala Ile
         419     215             220             225
E--> 421 ggg ctt ctc cca gct atg ctt ggc gga cag cca tat gtt gag gct caa
         422 955
         423 Gly Leu Leu Pro Ala Met Leu Gly Gly Gln Pro Tyr Val Glu Ala Gln
         424 230             235             240             245
E--> 426 gat ggt ctt tct gtt caa gaa tgg atg aaa aag cag ggc gta cct gaa
         427 1003
         428 Asp Gly Leu Ser Val Gln Glu Trp Met Lys Lys Gln Gly Val Pro Glu
         429             250             255             260
E--> 431 cgg gta gct gat gag gtg ttc ata gca atg tca aag gca cta aac ttc
         432 1051
         433 Arg Val Ala Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn Phe
         434             265             270             275
E--> 436 atc aat cct gat gaa ctt tca atg caa tgt ata ttg att gct tta aac
         437 1099
         438 Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu Asn
         439         280             285             290
E--> 441 cga ttt ctt cag gag aaa cat ggt tct aag atg gcc ttt ttg gat ggc
         442 1147
         443 Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp Gly
         444     295             300             305
E--> 446 aat cca ccc gaa aga ctt tgt atg cca ata gtt gat tat att cag tcc
         447 1195
         448 Asn Pro Pro Glu Arg Leu Cys Met Pro Ile Val Asp Tyr Ile Gln Ser
         449 310             315             320             325
E--> 451 ttg ggt ggt gaa gtt cat cta aat tcg cgc att caa aaa att gag cta
         452 1243
         453 Leu Gly Gly Glu Val His Leu Asn Ser Arg Ile Gln Lys Ile Glu Leu
         454             330             335             340
E--> 456 aat gat gat gga acg gtg aag agc ttc tta cta aat aat ggg aaa gtg
         457 1291
         458 Asn Asp Asp Gly Thr Val Lys Ser Phe Leu Leu Asn Asn Gly Lys Val
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E--> 463 atg gaa ggg gat gct tat gtg ttt gca act cca gtg gat att ctg aag
         464 1339
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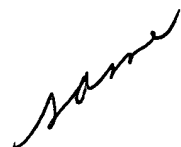
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      466         360             365             370
E--> 468 ctt ctt cta cca gat aac tgg aaa ggg att cca tat ttc cag aga ttg
      469 1387
      470 Leu Leu Leu Pro Asp Asn Trp Lys Gly Ile Pro Tyr Phe Gln Arg Leu
      471         375             380             385
E--> 473 gat aaa tta gtt ggc gtc cca gtc ata aat gtt cac ata tgg ttt gac
      474 1435
      475 Asp Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe Asp
      476 390             395             400             405
E--> 478 aga aaa ctg aag aac aca tat gat cac ctt ctc ttt agc aga agt ccc
      479 1483
      480 Arg Lys Leu Lys Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser Pro
      481             410             415             420
E--> 483 ctt ctg agt gta tat gct gac atg tca gta act tgc aag gaa tat tat
      484 1531
      485 Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr Tyr
      486         425             430             435
E--> 488 agc cca aac cag tca atg tta gag ttg gtt ttt gca cca gcc gaa gaa
      489 1579
      490 Ser Pro Asn Gln Ser Met Leu Glu Leu Val Phe Ala Pro Ala Glu Glu
      491         440             445             450
E--> 493 tgg att tca cgt agt gat gat gat att att caa gcc acg atg act gag
      494 1627
      495 Trp Ile Ser Arg Ser Asp Asp Asp Ile Ile Gln Ala Thr Met Thr Glu
      496         455             460             465
E--> 498 ctt gcc aaa ctc ttt cct gat gaa att tct gca gac caa agc aaa gca
      499 1675
      500 Leu Ala Lys Leu Phe Pro Asp Glu Ile Ser Ala Asp Gln Ser Lys Ala
      501 470             475             480             485
E--> 503 aag att ctc aag tac cat gtt gtt aaa aca cca agg tcg gtt tac aaa
      504 1723
      505 Lys Ile Leu Lys Tyr His Val Val Lys Thr Pro Arg Ser Val Tyr Lys
      506             490             495             500
E--> 508 act gtt cca aat tgt gaa cct tgt cga ccc att caa aga tct cct ata
      509 1771
      510 Thr Val Pro Asn Cys Glu Pro Cys Arg Pro Ile Gln Arg Ser Pro Ile
      511             505             510             515
E--> 513 gaa ggt ttc tat tta gct gga gat tac aca aaa caa aaa tat tta gct
      514 1819
      515 Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu Ala
      516         520             525             530
E--> 520 tca atg gaa ggc gct gtt ctt tct ggg aag ctt tgt gca cag gct att
      521 1867
      522 Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ala Ile
      523         535             540             545
E--> 525 gta cag gat tct gag cta cta gct act cgg ggc cag aaa aga atg gct
      526 1915
      527 Val Gln Asp Ser Glu Leu Leu Ala Thr Arg Gly Gln Lys Arg Met Ala
```

```
        528 550                  555              560              565
E--> 530 aaa gca agt gtt gtg taa caaaaacaag aattgaaaga gtcatggtag
        531 1963
        532 Lys Ala Ser Val Val
        533                  570
E--> 535 agtacaggag catcatttca actttggcat tctttgtctg tggtcaggac tcaggagacc
        536 2023
E--> 538 ttcaacttta ttagttcata cgaataaaga aaggctcagc ttctgaaatt tagctgcacc
        539 2083
E--> 541 gtcgtcaact gtgtgcaata agctatacgg aacaaacgac atgtgtcaac tttaagtcag
        542 2143
E--> 544 cccattgttt tgttatcctc caattttctg gatcaatgtt tgtattggaa agaaatatgt
        545 2203
E--> 547 cattattcaa acttgtttat atccactttt tttatttatc aacatttgtc acaacctttc
        548 2263
E--> 550 gttgagtaaa aaaaaaaaaa aaaagaattc
        551 2293
        639 <210> SEQ ID NO: 5
        640 <211> LENGTH: 2264
        641 <212> TYPE: DNA
        642 <213> ORGANISM: Zea mays
        644 <220> FEATURE:
        645 <221> NAME/KEY: CDS
        646 <222> LOCATION: (351)..(2066)
        648 <400> SEQUENCE: 5
E--> 649 ctccaaatgc ggaggtctcg actcttctct cttcctccat ctttatcatc gccccacgta
        650 60
E--> 652 cacacccaat tcctcgcaac tgggctcccc cgcctccacg acactgcccc ccgtctcaag
        653 120
E--> 655 tccgccgcct ccattcttca gctctcctat cctccgccta gaatatcttc atcggtattt
        656 180
E--> 658 taccaacctg gatcaattta ctcacgatac tctgaagcgt atacatatgc catatgggaa
        659 240
E--> 661 atgacttcat agctgtgggt tgtcttatgg ctccttgaat ttgcagtagt ctgcctgtac
        662 300
E--> 664 ctattggctg aagcagagct gaccccact ttatcaagag ttgctcaacg atg gac
        665 356
        666                                                         Met Asp
        667                                                          1
E--> 669 act ggc tgc ctg tca tct atg aat att act gga gct agc cag aca aga
        670 404
        671 Thr Gly Cys Leu Ser Ser Met Asn Ile Thr Gly Ala Ser Gln Thr Arg
        672          5                  10                 15
E--> 674 tct ttt gcg ggg caa ctt cct cct cag aga tgt ttt gcg agt agt cac
        675 452
        676 Ser Phe Ala Gly Gln Leu Pro Pro Gln Arg Cys Phe Ala Ser Ser His
        677     20                 25                 30
E--> 679 tat aca agc ttt gcc gtg aaa aaa ctt gtc tca agg aat aaa gga agg
        680 500
```

RAW SEQUENCE LISTING   DATE: 01/28/2005
PATENT APPLICATION: US/10/521,478   TIME: 11:37:36

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\01282005\J521478.raw

```
        681 Tyr Thr Ser Phe Ala Val Lys Lys Leu Val Ser Arg Asn Lys Gly Arg
        682 35                  40                  45                  50
E--> 684 aga tca cac cgt aga cat cct gcc ttg cag gtt gtc tgc aag gat ttt
        685 548
        686 Arg Ser His Arg Arg His Pro Ala Leu Gln Val Val Cys Lys Asp Phe
        687             55              60                  65
E--> 689 cca aga cct cca cta gaa agc aca ata aac tat ttg gaa gct gga cag
        690 596
        691 Pro Arg Pro Pro Leu Glu Ser Thr Ile Asn Tyr Leu Glu Ala Gly Gln
        694             70                  75                  80
E--> 696 ctc tct tca ttt ttt aga aac agc gaa cgc ccc agt aag ccg ttg cag
        697 644
        698 Leu Ser Ser Phe Phe Arg Asn Ser Glu Arg Pro Ser Lys Pro Leu Gln
        699             85                  90                  95
E--> 701 gtc gtg gtt gct ggt gca gga ttg gct ggt cta tca aca gcg aag tat
        702 692
        703 Val Val Val Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr
        704         100             105             110
E--> 706 ctg gca gat gct ggc cat aaa ccc ata ttg ctt gag gca aga gat gtt
        707 740
        708 Leu Ala Asp Ala Gly His Lys Pro Ile Leu Leu Glu Ala Arg Asp Val
        709 115             120                 125             130
E--> 711 ttg ggt gga aag gta gct gct tgg aag gat gaa gat gga gat tgg tac
        712 788
        713 Leu Gly Gly Lys Val Ala Ala Trp Lys Asp Glu Asp Gly Asp Trp Tyr
        714             135             140                 145
E--> 716 gag act ggg ctt cat ata ttt ttt gga gct tat ccc aac ata cag aat
        717 836
        718 Glu Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Ile Gln Asn
        719             150                 155                 160
E--> 721 ctg ttt ggc gag ctt agg att gag gat cgt ttg cag tgg aaa gaa cac
        722 884
        723 Leu Phe Gly Glu Leu Arg Ile Glu Asp Arg Leu Gln Trp Lys Glu His
        724         165                 170                 175
E--> 726 tct atg ata ttc gcc atg cca aac aag cca gga gaa ttc agc cgg ttc
        727 932
        728 Ser Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser Arg Phe
        729         180                 185                 190
E--> 731 gat ttc cca gaa act ttg cca gca cct ata aat ggg ata tgg gcc ata
        732 980
        733 Asp Phe Pro Glu Thr Leu Pro Ala Pro Ile Asn Gly Ile Trp Ala Ile
        734 195             200                 205                 210
E--> 736 ttg aga aac aat gaa atg ctt act tgg ccg gag aag gtg aag ttt gca
        737 1028
        738 Leu Arg Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Lys Phe Ala
        739             215                 220                 225
E--> 741 atc gga ctt ctg cca gca atg gtt ggt ggt caa cct tat gtt gaa gct
        742 1076
        743 Ile Gly Leu Leu Pro Ala Met Val Gly Gly Gln Pro Tyr Val Glu Ala
```

```
        744              230               235                240
E--> 746 caa gat ggc tta acc gtt tca gaa tgg atg aaa aag cag ggt gtt cct
     747 1124
     748 Gln Asp Gly Leu Thr Val Ser Glu Trp Met Lys Lys Gln Gly Val Pro
     749              245               250                255
E--> 753 gat cgg gtg aac gat gag gtt ttt att gca atg tcc aag gca ctc aat
     754 1172
     755 Asp Arg Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn
     756      260               265                270
E--> 758 ttc ata aat cct gat gag cta tct atg cag tgc att ttg att gct ttg
     759 1220
     760 Phe Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu
     761 275               280                285                290
E--> 763 aac cga ttt ctt cag gag aag cat ggt tct aaa atg gca ttc ttg gat
     764 1268
     765 Asn Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp
     766              295               300                305
E--> 768 ggt aat ccg cct gaa agg cta tgc atg cct att gtt gat cac att cgg
     769 1316
     770 Gly Asn Pro Pro Glu Arg Leu Cys Met Pro Ile Val Asp His Ile Arg
     771              310               315                320
E--> 773 tct agg ggt gga gag gtc cgc ctg aat tct cgt att aaa aag ata gag
     774 1364
     775 Ser Arg Gly Gly Glu Val Arg Leu Asn Ser Arg Ile Lys Lys Ile Glu
     776              325               330                335
E--> 778 ctg aat cct gat gga act gta aaa cac ttc gca ctt agt gat gga act
     779 1412
     780 Leu Asn Pro Asp Gly Thr Val Lys His Phe Ala Leu Ser Asp Gly Thr
     781      340               345                350
E--> 783 caa ata act gga gat gct tat gtt tgt gca aca cca gtc gat atc ttc
     784 1460
     785 Gln Ile Thr Gly Asp Ala Tyr Val Cys Ala Thr Pro Val Asp Ile Phe
     786 355               360                365                370
E--> 788 aag ctt ctt gta cct caa gag tgg agt gaa att act tat ttc aag aaa
     789 1508
     790 Lys Leu Leu Val Pro Gln Glu Trp Ser Glu Ile Thr Tyr Phe Lys Lys
     791              375               380                385
E--> 793 ctg gag aag ttg gtg gga gtt cct gtt atc aat gtt cat ata tgg ttt
     794 1556
     795 Leu Glu Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe
     796              390               395                400
E--> 798 gac aga aaa ctg aac aac aca tat gac cac ctt ctt ttc agc agg agt
     799 1604
     800 Asp Arg Lys Leu Asn Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser
     801      405               410                415
E--> 803 tca ctt tta agt gtc tat gca gac atg tca gta acc tgc aag gaa tac
     804 1652
     805 Ser Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr
     806      420               425                430
```

RAW SEQUENCE LISTING   DATE: 01/28/2005
PATENT APPLICATION: US/10/521,478   TIME: 11:37:36

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\01282005\J521478.raw

```
E--> 810 tat gac cca aac cgt tca atg ctg gag ttg gtc ttt gct cct gca gac
     811 1700
     812 Tyr Asp Pro Asn Arg Ser Met Leu Glu Leu Val Phe Ala Pro Ala Asp
     813 435               440           445               450
E--> 815 gaa tgg att ggt cga agt gac act gaa atc atc gat gca act atg gaa
     816 1748
     817 Glu Trp Ile Gly Arg Ser Asp Thr Glu Ile Ile Asp Ala Thr Met Glu
     818               455           460               465
E--> 820 gag cta gcc aag tta ttt cct gat gaa att gct gct gat cag agt aaa
     821 1796
     822 Glu Leu Ala Lys Leu Phe Pro Asp Glu Ile Ala Ala Asp Gln Ser Lys
     823               470           475               480
E--> 825 gca aag att ctt aag tat cat att gtg aag aca ccg aga tcg gtt tac
     826 1844
     827 Ala Lys Ile Leu Lys Tyr His Ile Val Lys Thr Pro Arg Ser Val Tyr
     828           485               490               495
E--> 830 aaa act gtc cca aac tgt gag cct tgc cgg cct ctc caa agg tca cct
     831 1892
     832 Lys Thr Val Pro Asn Cys Glu Pro Cys Arg Pro Leu Gln Arg Ser Pro
     833     500               505               510
E--> 835 atc gaa ggt ttc tat cta gct ggt gat tac aca aag cag aaa tac ctg
     836 1940
     837 Ile Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu
     838 515               520           525               530
E--> 840 gct tct atg gaa ggt gca gtc cta tcc ggg aag ctt tgt gcc cag tcc
     841 1988
     842 Ala Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ser
     843               535           540               545
E--> 845 ata gtg cag gat tat agc agg ctc gca ctc agg agc cag aaa agc cta
     846 2036
     847 Ile Val Gln Asp Tyr Ser Arg Leu Ala Leu Arg Ser Gln Lys Ser Leu
     848               550           555               560
E--> 850 caa tca gga gaa gtt ccc gtc cca tct tag ttgtagttgg ctttagctat
     851 2086
     852 Gln Ser Gly Glu Val Pro Val Pro Ser
     853           565               570
E--> 855 cgtcatcccc actgggtgct atcttatctc ctatttcaat gggaacccac ccaatggtca
     856 2146
E--> 858 tgttggagac aacacctgtt atggtccttt gaccatctcg tggtgactgt agttgatgtc
     859 2206
E--> 861 atattcggat atatatgtaa aaggacctgc atagcaattg ttagaccttg gaaaaaaa
     862 2264
     950 <210> SEQ ID NO: 7
     951 <211> LENGTH: 2027
     952 <212> TYPE: DNA
     953 <213> ORGANISM: Oryza sativa
     955 <220> FEATURE:
     956 <221> NAME/KEY: CDS
     957 <222> LOCATION: (5)..(1705)
```

RAW SEQUENCE LISTING   DATE: 01/28/2005
PATENT APPLICATION: US/10/521,478   TIME: 11:37:36

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\01282005\J521478.raw

```
      959 <400> SEQUENCE: 7
E--> 960 gttt atg aca gca tct gcc aga tat ttt gca gga caa ctt cct act cat
      961 49
      962      Met Thr Ala Ser Ala Arg Tyr Phe Ala Gly Gln Leu Pro Thr His
      963        1             5              10                    15
E--> 965 agg tgc ttc gca agt agc agc atc caa gca ctg aaa ggt agt cag cat
      966 97
      967 Arg Cys Phe Ala Ser Ser Ser Ile Gln Ala Leu Lys Gly Ser Gln His
      968               20              25                    30
E--> 970 gtg agc ttt gga gtg aaa tct ctt gtc tta agg aat aaa gga aaa aga
      971 145
      972 Val Ser Phe Gly Val Lys Ser Leu Val Leu Arg Asn Lys Gly Lys Arg
      973               35              40                    45
E--> 975 ttc cgt cgg agg ctc ggt gct cta cag gtt gtt tgc cag gac ttt cca
      976 193
      977 Phe Arg Arg Arg Leu Gly Ala Leu Gln Val Val Cys Gln Asp Phe Pro
      978           50              55              60
E--> 980 aga cct cca cta gaa aac aca ata aac ttt ttg gaa gct gga caa cta
      981 241
      984 Arg Pro Pro Leu Glu Asn Thr Ile Asn Phe Leu Glu Ala Gly Gln Leu
      985       65              70              75
E--> 987 tcc tca ttt ttc aga aac agt gaa caa ccc act aaa cca tta cag gtc
      988 289
      989 Ser Ser Phe Phe Arg Asn Ser Glu Gln Pro Thr Lys Pro Leu Gln Val
      990 80              85              90                    95
E--> 992 gtg att gct gga gca gga tta gct ggt tta tca acg gca aaa tat ctg
      993 337
      994 Val Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr Leu
      995               100             105             110
E--> 997 gca gat gct ggt cat aaa ccc ata ttg ctt gag gca agg gat gtt ttg
      998 385
      999 Ala Asp Ala Gly His Lys Pro Ile Leu Leu Glu Ala Arg Asp Val Leu
     1000           115             120             125
E--> 1002 ggt gga aag ata gct gct tgg aag gat gaa gat gga gat tgg tat gaa
     1003 433
     1004 Gly Gly Lys Ile Ala Ala Trp Lys Asp Glu Asp Gly Asp Trp Tyr Glu
     1005           130             135             140
E--> 1007 act ggg ctt cat atc ttt ttt gga gct tat ccc aac ata cag aac ttg
     1008 481
     1009 Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Ile Gln Asn Leu
     1010       145             150             155
E--> 1012 ttt ggc gag ctt ggt att aat gat cgg ttg caa tgg aag gaa cac tcc
     1013 529
     1014 Phe Gly Glu Leu Gly Ile Asn Asp Arg Leu Gln Trp Lys Glu His Ser
     1015 160             165             170                    175
E--> 1017 atg ata ttt gcc atg cca aac aag cca gga gaa tcc agc cgg ttt gat
     1018 577
     1019 Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Ser Ser Arg Phe Asp
     1020           180             185                    190
```

```
E--> 1022 ttt cct gaa aca ttg cct gca ccc tta aat gga ata tgg gcc ata cta
     1023 625
     1024 Phe Pro Glu Thr Leu Pro Ala Pro Leu Asn Gly Ile Trp Ala Ile Leu
     1025         195             200             205
E--> 1027 aga aac aat gaa atg cta act tgg cca gag aag gtg aag ttt gct ctt
     1028 673
     1029 Arg Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Lys Phe Ala Leu
     1030         210             215             220
E--> 1032 gga ctt ttg cca gca atg gtt ggt ggc caa gct tat gtt gaa gct caa
     1033 721
     1034 Gly Leu Leu Pro Ala Met Val Gly Gly Gln Ala Tyr Val Glu Ala Gln
     1035         225             230             235
E--> 1037 gat ggt ttt act gtt tct gag tgg atg aaa aag cag ggt gtt cct gat
     1038 769
     1039 Asp Gly Phe Thr Val Ser Glu Trp Met Lys Lys Gln Gly Val Pro Asp
     1042 240             245             250             255
E--> 1044 cga gtg aac gat gaa gtt ttc att gca atg tca aag gca ctt aat ttc
     1045 817
     1046 Arg Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn Phe
     1047         260             265             270
E--> 1049 ata aat cct gat gag tta tcc atg cag tgc att ctg att gct tta aac
     1050 865
     1051 Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu Asn
     1052         275             280             285
E--> 1054 cga ttt ctt cag gag aag cat ggt tct aag atg gca ttc ttg gat ggt
     1055 913
     1056 Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp Gly
     1057         290             295             300
E--> 1059 aat cct cct gaa agg tta tgc atg cct att gtt gac cat gtt cgc tct
     1060 961
     1061 Asn Pro Pro Glu Arg Leu Cys Met Pro Ile Val Asp His Val Arg Ser
     1062         305             310             315
E--> 1064 ttg ggt ggt gag gtt cgg ctg aat tct cgt att cag aaa ata gaa ctt
     1065 1009
     1066 Leu Gly Gly Glu Val Arg Leu Asn Ser Arg Ile Gln Lys Ile Glu Leu
     1067 320             325             330             335
E--> 1069 aat cct gat gga aca gtg aaa cac ttt gca ctt acc gat gga act caa
     1070 1057
     1071 Asn Pro Asp Gly Thr Val Lys His Phe Ala Leu Thr Asp Gly Thr Gln
     1072         340             345             350
E--> 1074 ata act gga gat gct tat gtt ttt gca aca cca gtt gat atc ttg aag
     1075 1105
     1076 Ile Thr Gly Asp Ala Tyr Val Phe Ala Thr Pro Val Asp Ile Leu Lys
     1077         355             360             365
E--> 1079 ctt ctt gta cct caa gag tgg aaa gaa ata tct tat ttc aag aag ctg
     1080 1153
     1081 Leu Leu Val Pro Gln Glu Trp Lys Glu Ile Ser Tyr Phe Lys Lys Leu
     1082         370             375             380
E--> 1084 gag aag ttg gtg gga gtt cct gtt ata aat gtt cat ata tgg ttt gat
```

```
        1085 1201
        1086 Glu Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe Asp
        1087     385             390             395
E--> 1089 aga aaa ctg aag aac aca tat gac cac ctt ctt ttc agc agg agt tca
        1090 1249
        1091 Arg Lys Leu Lys Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser Ser
        1092 400             405             410             415
E--> 1094 ctt tta agt gtt tat gcg gac atg tca gta act tgc aag gaa tac tat
        1095 1297
        1096 Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr Tyr
        1097             420             425             430
E--> 1101 gat cca agc cgt tca atg ctg gag ttg gtc ttt gct cct gca gag gaa
        1102 1345
        1103 Asp Pro Ser Arg Ser Met Leu Glu Leu Val Phe Ala Pro Ala Glu Glu
        1104             435             440             445
E--> 1106 tgg gtt gga cgg agt gac act gaa atc atc gaa gca act atg caa gag
        1107 1393
        1108 Trp Val Gly Arg Ser Asp Thr Glu Ile Ile Glu Ala Thr Met Gln Glu
        1109             450             455             460
E--> 1111 cta gcc aag cta ttt cct gat gaa att gct gct gat cag agt aaa gca
        1112 1441
        1113 Leu Ala Lys Leu Phe Pro Asp Glu Ile Ala Ala Asp Gln Ser Lys Ala
        1114     465             470             475
E--> 1116 aag att ctg aag tat cat gtt gtg aag aca cca aga tct gtt tac aag
        1117 1489
        1118 Lys Ile Leu Lys Tyr His Val Val Lys Thr Pro Arg Ser Val Tyr Lys
        1119 480             485             490             495
E--> 1121 act atc ccg gac tgt gaa cct tgc cga cct ctg caa aga tca ccg att
        1122 1537
        1123 Thr Ile Pro Asp Cys Glu Pro Cys Arg Pro Leu Gln Arg Ser Pro Ile
        1124             500             505             510
E--> 1126 gaa ggg ttc tat cta gct ggt gac tac aca aag cag aaa tat ttg gct
        1127 1585
        1128 Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu Ala
        1129             515             520             525
E--> 1131 tcg atg gag ggt gca gtt cta tct ggg aag ctt tgt gct cag tct gta
        1132 1633
        1133 Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ser Val
        1134             530             535             540
E--> 1136 gtg gag gat tat aaa atg cta tct cgt agg agc ctg aaa agt ctg cag
        1137 1681
        1138 Val Glu Asp Tyr Lys Met Leu Ser Arg Arg Ser Leu Lys Ser Leu Gln
        1139     545             550             555
E--> 1141 tcc gaa gtt cct gtt gcc tcc tag ttgtagtcag gactattccc aatggtgtgt
        1142 1735
        1143 Ser Glu Val Pro Val Ala Ser
        1144 560             565
E--> 1146 gtgtcatcat cccctagtca gttttttct atttagtggg tgcccaactc tccaccaatt
        1147 1795
```

```
E--> 1149 tacacatgat ggaacttgaa agatgcctat tttggtctta tcatatttct gtaaagttga
     1150 1855
E--> 1152 tttgtgactg agagctgatg ccgatatgcc acgctggaga aaaagaacat tatgtaaaac
     1153 1915
E--> 1157 gacctgcata gtaattctta gacttttgca aaaggcaaaa ggggtaaagc gacctttttt
     1158 1975
E--> 1160 ttctatgtga agggattaag agaccttaaa aaaaaaaaaa aaaaaaaaaa aa
     1161 2027
```

sane

VERIFICATION SUMMARY DATE: 01/28/2005
PATENT APPLICATION: **US/10/521,478** TIME: 11:37:37

Input Set : **A:\PTO.YF.txt**
Output Set: **N:\CRF4\01282005\J521478.raw**

```
L:13 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:15 M:270 C: Current Application Number differs, Replaced Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
M:254 Repeated in SeqNo=1
L:333 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
M:254 Repeated in SeqNo=3
L:649 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:5
M:254 Repeated in SeqNo=5
L:960 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:49 SEQ:7
M:254 Repeated in SeqNo=7
```